

Serial Number: 07/371,333/1

ENTERED

Changed a file from non-ASCII to ASCII

1646

#7

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____.

Added the mandatory heading and subheadings for "Current Application Data":

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included: _____

Deleted extra, invalid, headings used by an applicant, specifically: _____

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically: _____

Corrected an obvious error in the response, specifically: _____

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically: _____

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/371,333A DATE: 03/05/2001
 TIME: 14:42:25

Input Set : A:\Pto.vsk
 Output Set: N:\CRF3\03052001\I371333A.raw

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3 <110> APPLICANT: Xu, Wenfeng
4     Presnell, Scott R.
5     Yee, David P.
6     Foster, Donald C.
8 <120> TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PAR4
9     (ZCHEMR2)
11 <130> FILE REFERENCE: 98-10D1
13 <140> CURRENT APPLICATION NUMBER: US 09/371,333A
14 <141> CURRENT FILING DATE: 1999-08-10
16 <150> PRIOR APPLICATION NUMBER: US 09/053,866
17 <151> PRIOR FILING DATE: 1998-04-01
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4895
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (176)...(1330)
32 <400> SEQUENCE: 1
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34 tggtttatct ccaccggcgc gatctgctcg tccggctcgg ctccagaagc tggggctcag 120
35 ggtccggcga ggcaggaaac agccctgatg cagtc atg 178
36                                         Met
37                                         1
39 tgg ggg cga ctg ctc ctg tgg ccc ctg gtc agc ctg tct 226
40 Trp Gly Arg Leu Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu Ser
41      5          10          15
43 ggc ggc acc cag acc ccc agc gtc tac gac gag agc ggg agc acc gga 274
44 Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr Gly
45      20          25          30
47 ggt ggt gat gac agc acg ccc tca atc ctg cct gcc ccc cgc ggc tac 322
48 Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly Tyr
49      35          40          45
51 cca ggc caa gtc tgt gcc aat gac agt gac acc ctg gag ctc ccg gac 370
52 Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro Asp
53      50          55          60          65
55 agc tca cgg gca ctg ctt ctg ggc tgg gtg ccc acc agg ctg gtg ccc 418
56 Ser Ser Arg Ala Leu Leu Gly Trp Val Pro Thr Arg Leu Val Pro
57      70          75          80
59 gcc ctc tat ggg ctg gtc ctg gtg ggg ctg ccg gcc aat ggg ctg 466
60 Ala Leu Tyr Gly Leu Val Leu Val Gly Leu Pro Ala Asn Gly Leu
61      85          90          95
63 gcg ctg tgg gtg ctg gcc acg cag gca cct cgg ctg ccc tcc acc atg 514
64 Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr Met
65      100         105         110

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67	ctg	ctg	atg	aac	ctc	gcf	act	gct	gac	ctc	ctg	ctg	gcc	ctg	gcf	ctg		562
68	Leu	Leu	Met	Asn	Leu	Ala	Thr	Ala	Asp	Leu	Leu	Leu	Ala	Leu	Ala	Leu		
69	115				120					125								
71	ccc	ccg	cgg	atc	gcc	tac	cac	ctg	cgt	ggc	cag	cgc	tgg	ccc	ttc	ggg		610
72	Pro	Pro	Arg	Ile	Ala	Tyr	His	Leu	Arg	Gly	Gln	Arg	Trp	Pro	Phe	Gly		
73	130				135					140			145					
75	gag	gcc	gcc	tgc	cgc	ctg	gcc	acg	gcc	qca	ctc	tat	ggt	cac	atg	tat		658
76	Glu	Ala	Ala	Cys	Arg	Leu	Ala	Thr	Ala	Ala	Leu	Tyr	Gly	His	Met	Tyr		
77	150				155					160								
79	ggc	tca	gtg	ctg	ctg	ctg	gcc	gtc	agc	ctg	gat	cyc	tac	ctg	gcc		706	
80	Gly	Ser	Val	Leu	Leu	Leu	Ala	Ala	Val	Ser	Leu	Asp	Arg	Tyr	Leu	Ala		
81	165				170					175								
83	ctg	gtg	cac	ccg	ctg	cgg	gcc	cgc	ctg	cgt	ggc	cgg	cgc	ctg	gcc		754	
84	Leu	Val	His	Pro	Ieu	Arg	Ala	Arg	Ala	Leu	Arg	Gly	Arg	Arg	Leu	Ala		
85	180				185					190								
87	ctt	gga	ctc	tgc	atg	gct	gct	tgg	ctc	atg	gcf	gcc	gcc	ctg	gca	ctg		802
88	Leu	Gly	Leu	Cys	Met	Ala	Ala	Trp	Leu	Met	Ala	Ala	Leu	Ala	Leu			
89	195				200					205								
91	ccc	ctg	aca	ctg	cag	cgg	cag	acc	ttc	cgg	ctg	gcf	cgc	tcc	gat	cgc		850
92	Pro	Leu	Thr	Leu	Gln	Arg	Gln	Thr	Phe	Arg	Leu	Ala	Arg	Ser	Asp	Arg		
93	210				215					220			225					
95	gtg	ctc	tgc	cat	gac	gcf	ctg	ccc	ctg	gac	gca	cag	gcc	tcc	cac	tgg		898
96	Val	Leu	Cys	His	Asp	Ala	Leu	Pro	Leu	Asp	Ala	Gln	Ala	Ser	His	Trp		
97	230				235					240								
99	caa	ccg	gcc	ttc	acc	tgc	ctg	gcf	ctg	tgg	gyc	tgt	ttc	ctg	ccc	ctg		946
100	Gln	Pro	Ala	Phe	Thr	Cys	Leu	Ala	Leu	Leu	Gly	Cys	Phe	Leu	Pro	Leu		
101	245				250					255								
103	ctg	gcc	atg	ctg	ctg	tgc	tac	ggg	gcc	acc	ctg	cac	acg	ctg	gcf	gcc		994
104	Leu	Ala	Met	Leu	Leu	Cys	Tyr	Gly	Ala	Thr	Leu	His	Thr	Leu	Ala	Ala		
105	260				265					270								
106	agc	ggc	cgg	cgc	tac	ggc	cac	gcf	ctg	agg	ctg	acc	gca	gtg	gtg	ctg		1042
107	Ser	Gly	Arg	Arg	Tyr	Gly	His	Ala	Leu	Arg	Leu	Thr	Ala	Val	Val	Leu		
108	275				280					285								
110	gcc	tcc	gcc	gtg	gcc	ttc	ttc	gtg	ccc	agc	aac	ctg	ctg	ctg	ctg	ctg		1090
111	Ala	Ser	Ala	Val	Ala	Phe	Phe	Val	Pro	Ser	Asn	Leu	Leu	Leu	Leu			
112	290				295					300			305					
114	cat	tac	tgc	gac	ccg	agg	ccc	agc	gcc	tgg	ggc	aac	ctc	tat	ggt	gcc		1138
115	His	Tyr	Ser	Asp	Pro	Ser	Pro	Ser	Ala	Trp	Gly	Asn	Leu	Tyr	Gly	Ala		
116	310				315					320								
118	tac	gtg	ccc	agc	ctg	gcf	ctg	agc	acc	ctc	aat	agc	tgc	gtg	gat	ccc		1186
119	Tyr	Val	Pro	Ser	Ieu	Ala	Leu	Ser	Thr	Ieu	Asn	Ser	Cys	Val	Asp	Pro		
120	325				330					335								
122	ttc	atc	tac	tac	gtg	tgc	gcc	gag	ttc	agg	gac	aag	gtg	cgf	gca		1234	
123	Phe	Ile	Tyr	Tyr	Tyr	Val	Ser	Ala	Glu	Phe	Arg	Asp	Lys	Val	Arg	Ala		
124	340				345					350								
126	ggg	ctc	tcc	caa	ccg	tgc	ccg	ggg	gac	acc	gtg	gcc	tcc	aag	gcc	tct		1282
127	Gly	Leu	Phe	Gln	Arg	Ser	Pro	Gly	Asp	Thr	Val	Ala	Ser	Lys	Ala	Ser		
128	355				360					365								
130	gcf	gaa	ggg	ggc	agc	ccg	ggc	atg	ggc	acc	cac	tcc	tct	tgt	ctc	cag		1330

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Input Set : A:\Pto.vsk
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181 gctcgacccg gcccaggagg cccggggcgc ttagtcagg cccagaactg gctgattca 4210
182 gggataccca ggacgcgtga aacacagaag aaacgtgatc ccattttctt tttttcttt 4270
183 actttttctt tttttttttt ttctctgagac agagtctcgc gctgtgccc aggctggagt 4330
184 gcagtggcgt gatctcggt cactgraage tcggctctt gggttcaaat gattctctg 4390
185 cttcagccctt ccaaytagct ggatatacag gggcccacca cccgccccctt ctaatttt 4450
186 gtatttttga tcaagacgga gtttcaccaat gttggccagg ctggcttcca acttcgtccc 4510
187 tcaagtgatc cgccctggtc ccatttttta ttctttgggt ctttccatcc cactggaaa 4570
188 acgtctcagg tggectctga aacaccactt ctttttgtgt gtgtgcacgc atggctgac 4630
189 atgtgtgggt gggatcgac acattcacga tactgtgaa tcatcaccc tgcgttagtt 4690
190 caggacgggtt tcttttccc ccaaagaaac cccatcgcca tcagcacca ctccccactc 4750
191 ccccaaaaaaa tggcaaccac aaatctttcc aactctacgg atttgcgtt tctgggcatt 4810
192 tcatgtcaat ggaatcatgt actctgtgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4870
193 aaaaaaaaaa aaaaaaaaaa aaaaa 4895

195 <210> SEQ ID NO: 2
196 <211> LENGTH: 385
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 2
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202 1 5 10 15
203 Ser Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr
204 20 25 30
205 Gly Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly
206 35 40 45
207 Tyr Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro
208 50 55 60
209 Asp Ser Ser Arg Ala Leu Leu Gly Trp Val Pro Thr Arg Leu Val
210 65 70 75 80
211 Pro Ala Leu Tyr Gly Leu Val Leu Val Gly Leu Pro Ala Asn Gly
212 85 90 95
213 Leu Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr
214 100 105 110
215 Met Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu Ala
216 115 120 125
217 Leu Pro Pro Arg Ile Ala Tyr His Leu Arg Gly Gln Arg Trp Pro Phe
218 130 135 140
219 Gly Glu Ala Ala Cys Arg Leu Ala Thr Ala Ala Leu Tyr Gly His Met
220 145 150 155 160
221 Tyr Gly Ser Val Leu Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu
222 165 170 175
223 Ala Leu Val His Pro Leu Arg Ala Arg Ala Leu Arg Gly Arg Arg Leu
224 180 185 190
225 Ala Leu Gly Leu Cys Met Ala Ala Trp Leu Met Ala Ala Leu Ala
226 195 200 205
227 Leu Pro Leu Thr Leu Gln Arg Gln Thr Phe Arg Leu Ala Arg Ser Asp
228 210 215 220
229 Arg Val Leu Cys His Asp Ala Leu Pro Leu Asp Ala Gln Ala Ser His
230 225 230 235 240
231 Trp Gln Pro Ala Phe Thr Cys Leu Ala Leu Leu Gly Cys Phe Leu Pro
232

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233	245	250	255
234	Leu Leu Ala Met Leu Leu Cys Tyr Gly Ala Thr Leu His Thr Leu Ala		
235	260	265	270
236	Ala Ser Gly Arg Arg Tyr Gly His Ala Leu Arg Leu Thr Ala Val Val		
237	275	280	285
238	Leu Ala Ser Ala Val Ala Phe Phe Val Pro Ser Asn Leu Leu Leu		
239	290	295	300
240	Leu His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly		
241	305	310	315
242	Ala Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp		
243	325	330	335
244	Pro Phe Ile Tyr Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg		
245	340	345	350
246	Ala Gly Leu Phe Gln Arg Ser Pro Gly Asp Thr Val Ala Ser Lys Ala		
247	355	360	365
248	Ser Ala Glu Gly Gly Ser Arg Gly Met Gly Thr His Ser Ser Leu Leu		
249	370	375	380

250 Gln

251 385

253 <210> SEQ ID NO: 3

254 <211> LENGTH: 1155

255 <212> TYPE: DNA

256 <213> ORGANISM: Artificial Sequence

258 <220> FEATURE:

259 <223> OTHER INFORMATION: This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

260

262 <221> NAME/KEY: variation

263 <222> LOCATION: (1)...(1155) /

264 <223> OTHER INFORMATION: N is any nucleotide.

266 <400> SEQUENCE: 3

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W--> 268	caracncnw sngtnayga ygarwsnggn wsnaclngng gnggngayga ywsnaclncn	120
W--> 269	wsnathytnc cngcncnmg ngntayccn ggncaargtnt gygcnaayga ywsngayacn	180
W--> 270	ytngarytnc cngaywsnws nmgnccnytn ytnytnngnt gggtnccnac nmgnytngt	240
W--> 271	cncnytnyt ayggnytnyt nytnytngt ggnytnccng cnaayggnyt ncnytnntgg	300
W--> 272	gtnytnngna cnacrgcncc nmgnytnccn wsnaclnatgaa tnytnatgaa yytnngcna	360
W--> 273	gcnaytngt nytnytnccn ncnytnccn cncmgnathg cnytngtnta nmgnngncar	420
W--> 274	mgntggccnt tyggngargc ncnytngtnta ytnytnccn cngcnytnta yggncayatg	480
W--> 275	tayggnwsgn tnytnytnyt ncnytngtnta wsnytnytnym gntayytnyc nytnytnccay	540
W--> 276	ccnytnmngn cmgnccnyt nmgnngnmgn mgnytnccny tnngnytnyngt yatggcngcn	600
W--> 277	tggynatgg cngcngcnyt ncnytnccn ytnacnytnc armgnccarac nttyngnytn	660
W--> 278	gcnmghwsng aymngnytnyt ntgycaygay gcnytncn tngaygcna rgcnwsnacay	720
W--> 279	tggccarccng cnytngtnta ytnytnccn ytnytnccn ytnytnccn ytnytnccn	780
W--> 280	ytnytnccn ytnytnccn ytnytnccn ytnytnccn ytnytnccn ytnytnccn	840
W--> 281	gcnytnmgn tnaacngcngt ytnytnccn wsngcngtng cnytngtnta ytnytnccn	900
W--> 282	ytnytnytnyt nytnytnytnyt nytnytnytnyt nytnytnytnyt nytnytnytnyt	960
W--> 283	gcnytngn ytnytnytnyt nytnytnytnyt nytnytnytnyt nytnytnytnyt nytnytnytnyt	1020
W--> 284	taytaygtw sngcngartt ymgngayaar gtnmgnccng gnytnttyca rmgnwsnccn	1080
W--> 285	ggngayacng tngcnwsnaa rgcnwsnacn garggnggnw snmgnggnat gggnacnac	1140

VERIFICATION SUMMARY DATE: 03/05/2001
PATENT APPLICATION: US/09/371,333A TIME: 14:42:26

Input Set : A:\Pto.vsk
Output Set: N:\CRF3\03052001\I371333A.raw

L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3